

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaCAAQPaiHi: 995 aa

>SEQ ID NO:2

vs /tmp/fastaDAARPaiHi library

searching /tmp/fastaDAARPaiHi library

1008 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 39, opt: 27, gap-pen: -12/ -2, width: 16
Scan time: 0.050

The best scores are:

NM_000096 ACCESSION:NM_000096 NID: gi 4557484 ref (1008) 2671 opt

>>NM_000096 ACCESSION:NM_000096 NID: gi 4557484 ref NM_0 (1008 aa)

initn: 1414 initl: 972 opt: 2671

Smith-Waterman score: 3980; 57.002% identity in 1014 aa overlap (1-992:1-1008)

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      10      20      30      40      50
SEQ   MKILILGIFLFLCSPGWAIDRHCYIGIEESIWNYPSPGKNMLNEKPFSEDLE----FLQ
      .....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
NM_000 MKILILGIFLFLCSTPAWAKEKHYYIGIIEETTWDYA---SDHGEKKLISVDTEHSNIYLQ
      10      20      30      40      50

      60      70      80      90     100     110
SEQ   GGQARKSFVFKKALYFQYTDNTFQRIIEKPSWLGLGPMIKAETGDFIYVHVKNNASRAY
      ..:.....:.....:.....:.....:.....:.....:.....:.....:.....:
NM_000 NGPDRIGRLYKKALYLQYTDFTRTTIEKPVWLGLGPIIKAETGDKVYVHLKNLASRPY
      60      70      80      90     100     110

      120     130     140     150     160     170
SEQ   SYHPHGLTYSKENEAHGAIYPDNTTGLQKEVEYLEPGKQYTYKWYVEEHQGPSPNDNSNCV
      ..:.....:.....:.....:.....:.....:.....:.....:.....:.....:
NM_000 TFHSHGITYYKEHE--GAIYPDNTTDFQRADDKVYPGEQYTYMLLATEEQSPGEGDGNCV
      120     130     140     150     160     170

      180     190     200     210     220     230
SEQ   TRIYHSHIDTARDVASGLIGPILTCKRGTNLNGDTEKDIDRSSFLMFSTTDESRSWYSDEN
      .....:.....:.....:.....:.....:.....:.....:.....:.....:
NM_000 TRIYHSHIDAPKDIASGLIGPLIICKKDSLDKEKEKHIDREFVVMFSVVDENFSWYLEDN
      180     190     200     210     220     230

      240     250     260     270     280     290
SEQ   IRAF-TESGKINTSDPRFEESMSMQSINGYIYGNLPNLTMCAEDRVQWYFVGMGGVADIIH
      ....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
NM_000 IKTYCSEPEKVDKDNEFDQESNRMYSVNGYTFGSLPGLSMCAEDRVKWYLFMGMGNEVDVH
      240     250     260     270     280     290

      300     310     320     330     340     350
SEQ   PVYLRGQTLISRNHRKDTIMLFSSLEDAFMVAKAPGVWMLGCQ----IHESMQAFFFKVS
      .....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
NM_000 AAFHFHGQALTKNKYRIDTINLFPATLFDAYMVAQNPGEWMLSCQNLNHLKAGLQAFFQVQ
      300     310     320     330     340     350
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	360	370	380	390	400	410
SEQ	NCQKPST	EAFTV	TGTHVI	HYIIAA	KEILWNY	APSGIDFFTKKNLTAAGSKSQLFFERSPT
NM_000	ECNKSSSKDNIRGKHVRHYIIAAEEIIWNYAPSGIDIFTKENLTAPGSDSAVF	FEQGT	TTR			
	360	370	380	390	400	410
	420	430	440	450	460	
SEQ	IGGTYKKLIYREYTDASFQTQKAR--EEHLGILGPVFKA	EVGQT	IKITFYNNASLPLSI			
NM_000	IGGSYKKLVYREYTDASF	TNRKERGP	EEHLGILGPVIWA	EVGDTIRVTFHNKGAYPLSI		
	420	430	440	450	460	470
	470	480	490	500	510	520
SEQ	QPPGLHYNKSNEGLFYE---TPGG-STPPPS	SHVSPGTTFVYTWEV	PKDVGPTSTDPNCL			
NM_000	EPIGVRFNKNNEGTYSPNYPQSR	SVPPSASHVAPTETFTYEW	TVPKEVGPTNADPVCL			
	480	490	500	510	520	530
	530	540	550	560	570	580
SEQ	TWFYYSVNGKKDINSGLLGPLLICRNGSLGDDGKQKGV	DKEFYLLATIFDENESNLLDE				
NM_000	AKMYSAVDPTKDIFTGLIGPMKICKKGS	LHANGRQKDVDKEFYLFPTVFDENESLLED				
	540	550	560	570	580	590
	590	600	610	620	630	640
SEQ	N-RTFITEPENIDKEDTDCQASNK	MYRINGYMG	NLPGLD	TCLGDNVLWHVFSVGSVEDL		
NM_000	NIRMF	TTAPDQVDKED	EDFQESNKM	HSMNGFM	YGNQPG	LTMC
	600	610	620	630	640	650
	650	660	670	680	690	700
SEQ	HGIYFSGNTFTSLGAR	RD	TIPMF	PYTSQ	TLLMTPDSIGTFDLV	CMTIKHNLGGMKHKYHV
NM_000	HGIYFSGNTYLWRGER	RD	TANLFPQ	TS	TLHMWP	PDTEGTFNVECLTTDHYTGGMKQKYTV
	660	670	680	690	700	710
	710	720	730	740	750	760
SEQ	RQCGKPNPDQ	TQYQEEKIIITIAA	EE	MEWDYSPSRK	WENELHHLRRENQ	TSMYVDRSGL
NM_000	NQ	CRRQ	SEDSTFYLGERTY	-IAAVE	VEWDYSPQREWEKELHHLQEQNV	SNAFLDKGEFY
	720	730	740	750	760	770
	770	780	790	800	810	820
SEQ	LGSKYKKVLYRQYDDNTFT	NQTKRNEGEK	HL	DILGPLILLNP	GQIIQIIFKNKA	ARPYSI
NM_000	IGSKYKKVVYRQYTDST	FRVP	VERKAE	EEHLGILGPQLHAD	VGDVKIIFKN	MATRYPYSI
	780	790	800	810	820	830
	830	840	850	860	870	880
SEQ	HAHGVKTNNSTVVPTQ	PG	EIQIYT	WQIPDR	TGPTSLDFECIPWFY	YSTVSVAKDLHSGLV
NM_000	HAHGVQTESSTVTPTLP	GETLTYV	WKIPERSG	AGTEDSACIPWAY	YSTVDQVKDLYSGLI	
	840	850	860	870	880	890

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      890      900      910      920      930
SEQ   GPLSVCR----KDINPN-IVHRVLHFMIFDENESWYFEDSINTYASKPNKVDKENDNFQL
      :::  :::  :  :::  ..  .:  .....:
NM_000 GPLIVCRRPYLKVFNP RRKLEFALLFLVFDENESWYLD DNIKTYS DHPEKVNKDDEEFIE
      900      910      920      930      940      950

      940      950      960      970      980      990
SEQ   SNQMHAINGRLFGNNQGITFHVGDVVNWYLGIGNEADLHTVHFHGHHSFEYKHKYLI
      .....: .....: .....: .....: .....:
NM_000 SNKMHAINGRMFGNLQGLTMHVGDEVNWYLMGMGNEIDLHTVHFHGHHSFQYKHR
      960      970      980      990      1000

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995 residues in 1 query sequences

1008 residues in 1 library sequences

Scomplib [version 3.3t05 March 30, 2000]

start: Wed Sep 18 11:16:31 2002 done: Wed Sep 18 11:16:32 2002

Scan time: 0.050 Display time: 1.417

Function used was FASTA